

Molecular mechanism of BASIC PENTACYSTEINE factors (BPCs) and MADS-box transcription factor *SVP* involved in reproductive development in the model species *Arabidopsis thaliana*.

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The development of flower meristems and fruits are two extremely important agronomical traits. MADS-domain transcription factors (TFs) are key regulators of these processes and we are focusing on how these TFs and their interacting partners control the regulatory network leading to reproductive meristem formation and fruit development in the model plant *Arabidopsis thaliana*.

An excellent starting point for this research project is the large amount of information and tools that we and other groups have already generated for one of the key players in both vegetative and reproductive meristem development: the MADS-domain TF SHORT VEGETATIVE PHASE (SVP). SVP acts as a repressor of the floral transition in the vegetative meristem and later as a key factor floral meristem identity factor (Gregis et al., 2013). Moreover we have recently characterized the function of the complex composed of SVP and BASIC PENTACYSTEINE factors (BPCs) (Simonini et al., 2012). BPCs are transcription factors with affinity to GA-repeated sequences, involved in transcription regulation through their interaction with other TFs and chromatin modifiers. We showed that BPC binding sites are important for BPC recruitment to the DNA but also for binding of SVP to nearby MADS-domain binding sites (CArG boxes).

We focus our attention on the molecular mechanisms by which SVP and its interaction partners control their targets. MADS-domain factors have been studied deeply from a genetic point of view and are recognised as key controllers of development in plants. However, little is known about the molecular aspects (DNA binding mechanisms, recruitment of complex members etc.).

We are studying two important interconnected research lines that are related to the regulatory mechanisms that underlay reproductive development: (i) the mechanistic molecular aspects of target gene regulation by SVP and its interacting partners BPCs and (ii) the analysis of *bpc* multiple mutants combinations phenotype and the characterization of their role in fruit development.

Gregis et al., Genome Biol. 2013 Jun 11;14(6):R56. [Epub ahead of print]

Simonini et al., The Plant Cell 2012 (10):4163-72.